efflux-pump gene expressions (*marA, mdfA*) were also checked for the MDR isolates.

Results: Out of 453 samples screened for *E. coli*, 386 (85.2%) isolates was recovered, while 47 (7.03%) *Salmonella* was isolated from 668 samples examined. Above 6 percent *E. coli* showed resistance to all the tested antibiotics. Over 80 percent *Salmonella* were resistant to amikacin, cefazolin and tobramycin and other remaining exhibited high frequency of resistance against cefuroxime (74.5%) and gentamicin (68.1%). Overall *marA* gene was the most common type with 15 percent harboring the gene. Above 10.8 percent isolates possessed *sul1, sul2, tetA, strA* genes and above 5 percent carried *tetB, aadA, armA, bla$_{TEM}$ and bla$_{CTX-M}$*, however, *bla$_{SHV}$* gene, *armB* and *rmtC* were not recovered. Plasmid mediated quinolone resistant gene positive strains totaled to 4.4 (*qnrB*) and 2.07 (*qnrS*) percent while *qnrA* was not detected. Species and region-wise distributions were variable. Resistant traits were transferable and the resistant isolates had shown ≥2 fold increase in the expression level of *marA.* '

Conclusion: Emergence of MDR in *E. coli* or *Salmonella* among the animal populations of NE India was evident from the study revealing above 85 percent MDR isolates. These results emphasize the urgent need for surveillance of antibiotic resistance incorporating rational and regulated use of antibiotics in Livestock farming.

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Correlation of carbapenem resistance and hypermucoviscosity in K.pneumoniae isolated from blood culture at a tertiary hospital in South India

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Background: Carbapenem resistant *K.pneumoniae* (CRKp) are posing an increasing presenting a threat to treatment of infections especially in children and immunocompromised patients. Recently there are cases with hypervirulent/hypermucoviscous *K.pneumoniae* (hvKp) infections associated with high mortality rates of 52% and metastatic spread. Hence it is important to know the factors contributing to disease severity in hvKp infections. There are limited reports regarding carbapenem susceptibility of hvKp which however is an important factor contributing to patient outcome. We aimed at studying the prevalence of genes coding for carbapenamases among hvKp and distribution of meropenem MIC among hvKp and non-hvKp.

Methods & Materials: A total of 77 CRKp isolated from blood culture during 2014 and 2015 at department of Clinical Microbiology, CMC, were included. Screening for carbapenem resistance was done by disc diffusion method for susceptibility to imipenem and meropenem and resistant isolates were included which were then subjected to E-test for meropenem. The results for antimicrobial susceptibility testing were interpreted according to CLSI guidelines. The resistant isolates were then subjected to string test which is the phenotypic test for hvKp, and multiplex PCR for detection of genes for carbapenemase production.

Results: Among the 77 CRKp isolates tested, 25 (32%) were string test positive and 52 (68%) were negative. The majority of hvKp, 10 (40%), co-expressed NDM and OXA48-like genes while 19 (37%) non-hvKp expressed OXA48-like. Meropenem MIC range obtained was 0.064 μg/ml - >32 μg/ml. 72% and 65% of hvKp and non-hvKp had MIC of ≥32 μg/ml. Overall, OXA48-like genes were the most predominant genes isolated from 25 (32%) isolates tested.

Conclusion: Co-expression of NDM and OXA48-like genes might contribute to the increased MIC for meropenem among the hvKp which is a potential threat for patient management. Monitoring the frequency of isolation and susceptibility profile for hvKp will help in achieving clinical cure by administering the right antibiotic and prevention of metastatic spread of infection. Decreased susceptibility and the hypermucoviscous nature might contribute to the severity of infection and increased mortality in infections with hvKp than the classical *K.pneumoniae*.

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Prevalence and antibiogram of pseudomonas aeruginosa isolated from clinical specimens in a Teaching Hospital, Kathmandu

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Background: *Pseudomonas aeruginosa* is a leading cause of nosocomial infections. Increased resistance in this organism continues to pose a significant threat to patient care because of limited therapeutic options. Knowledge of the prevalence of *P. aeruginosa* in various infections and their antibiotic susceptibility pattern is of utmost importance for selection of appropriate therapy. Objective of the present study was to determine the prevalence and resistance pattern of *P. aeruginosa* isolated from various clinical specimens to Imipenem and other commonly used antibiotics in Nepal Medical College and Teaching Hospital (NMCTH), a teaching hospital in Kathmandu, Nepal.

Methods & Materials: *P. aeruginosa* isolated from various clinical specimens like pus, sputum, blood, urine, catheter tips (devices), renal stones and body fluids processed in the clinical laboratory, department of Microbiology, NMCTH were included in the study. Isolation, Identification and antimicrobial susceptibility pattern were performed using standard microbiological techniques.

Results: A total of 102 isolates of *P. aeruginosa* were evaluated. The prevalence rate of the organism was 5.1%, out of which 75 (73.5%) were from inpatients and 27 (26.5%) were from outpatients departments. Urine and sputum yielded highest number of the isolates 37 (36.3%) each followed by pus and devices 10 (9.8%) each. Highest percentage of the organism 36 (35.3%) was isolated from the patients who were of more than 60 years of age. Nineteen (18.6%) of the organims was seen to be multi-drug resistant. The organism showed maximum resistance to Piperacillin (57.1%) followed by Ciprofloxacin (36.7%), Ofloxacin (28.8%) and Gentamycin (30.9%). Only 6.5% of the isolates were resistant to Imipenem.

Conclusion: The antibiotic susceptibility pattern of bacterial pathogen like P. aeruginosa in the hospital settings should be continuously monitored and the results readily made available to clinicians so as to maximize the possibility of administering an effective therapeutic agent whenever needed.

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Risk Factors for aquisition of invasive infections with NDM-1 $^{+}$ K. pneumoniae

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Background: Carbapenem resistance conferred by New Delhi metallo-βlactamase 1 (NDM-1) is an increasing global public health problem and defining risk factors for acquisition of infections with NDM-1 containing organisms is urgently needed for its control.

Methods & Materials: We investigated the patient and hospital related risk factors for acquisition of in patients at CMC Hospital infected with invasive *Klebsiella pneumoniae* with and without NDM-1. This was a retrospective case-control study of patients admitted at CMC Hospital, Vellore between Oct 2009 and Sept 2014, with blood culture + invasive *Klebsiella pneumonia* that were NDM-1^{+} (case), NDM-1^{-}ESBL^{+} (ESBL^{+} control), or NDM-1^{-}ESBL^{-} (ESBL^{-} control). Cases and controls were matched on date of admission ± 45 days.

Results: There were 101 NDM-1^{+}cases, and 100 ESBL^{+} and 101 ESBL^{-} controls, with little difference in mean ages: 31.20±22.94, 29.78±23.30, and 41.55±21.11, respectively. NDM-1^{+} subjects were more likely to have received antibiotics in the last 180 days than either the ESBL^{+} (*OR*= 1.478 [0.756-2.887]; *P*= .253) or ESBL^{-} (*OR*= 1.713 [.863-3.402]; *P* = 0.124) controls, and were more likely to have acquired the infection nosocomially than the ESBL^{+} (*OR*= 1.653 [0.861-3.174]; *P* = 0.131) and ESBL^{-} (*OR*= 3.390 [1.808-6.329]; *P* = <0.001). NDM-1^{+} patients were more likely than ESBL^{+} (*OR* =2.114 [1.202-3.719]; *P* = 0.01) and ESBL^{-} (*OR* =1.910 [1.088-3.352]; *P* = 0.024) to have been admitted to the ICU. The Case Fatality Ratio (CFR) was significantly higher in *NDM-1*$^{+}$ patients than in ESBL^{+} (2.26; *P* <0.001) and ESBL^{-} (3.8 *P* <0.001). The mean length of hospital stay for NDM-1^{+} patients was 31.30±31.827, and was significantly higher in than in ESBL^{+} (23.21±17.252; *P* = 0.001) and ESBL^{-} (19.68±18.55; *P* =0.002).

Conclusion: NDM-1^{+} *K.pneumoniae invasive* infections are as likely to be aquired in the community as nosocomially but in the latter circumstance are more likely to be aquired in the ICU.The CFR of 52% is twice that of ESBL^{+} invasive *Klebsiella.*

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Assessment of antibiotic resistance patterns of the fecal coliforms isolated from Cauvery River and screening of novel herbal lead molecules against probable drug targets of MDR pathogens by computational virtual screening

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Background: The present study focus elucidation of microbial pollution and antibiotic resistance profiling of bacteria isolated from River Cauvery. This study focused to screen herbal leads against probable drug targets of multidrug resistant isolates by computional virtual screening.

Methods & Materials: Water samples were collected during 2011-12 from ten hotspots. The physiochemical characteristics and microbial counts were determined. Kirby Bauer disc diffusion assay was used to investigate the antibiotic sensitivity profile of various isolates. Selected virulent toxins and gene products for bacterial drug resistance were identified as the probable drug targets. The 3D structures of these were predicted by homology modeling. The drug likeliness and pharmacokinetic properties of selected phytoligands were computationally predicted. The binding properties of ligands and drug targets were studied by molecular docking.

Results: The samples collected from all the hotspots showed high bacterial count (*P<0.01*). Out of 848 isolates, 93.51% (n=793) demonstrated multidrug resistance to most antibiotics. 96.46% (n=273), 93.85% (n=107), 94.49% (n=103), 90.22% (n=157) of the isolates were exhibited multi-drug resistance to 30, 32, 40, 37 antibiotics and they were identified to be *E.coli*, *Enterobacter cloacae*, *Pseudomonas trivialis* and *Shigella sonnei* respectively. The prevalence of bla_{TEM}, in all the four isolates and *dhfr* in *E.coli* and *Shigella sonnei* were identified. *Yokenella, Morganella, Citrobacter, Serratia, Salmonella, Proteus, Klebsiella, Edwersiella, Alcaligenes,Staphylococcus* and *Vibrio* were also showed multidrug resistance. This study suggested Cadinane and Cedrol showed good binding against shiga and cholera toxins respectively. Violaxanthin identified as therapeutic lead for hemolysin-E. Afzelin and gallocathecin were identified as lead against bla_{TEM} and *dhfr*. Baicalein and Luteolin were identified as leads against *aph* of *S.typhi.* Resveratrol and Wogonin were identified as leads against *dhfr* of *Salmonella typhi.* Herniarin and Pyrocide were identified as leads against *dfrA1* of *Vibrio cholerae*. Taraxacin and Luteolin against *mec1* and Apigenin and Luteolin against *vanH* of *Staphylococcus aureus* as therapeutic leads.

Conclusion: The current study showed predominance of many multidrug-resistant bacteria in River Cauvery. Bionformatics study suggests that phytoligands present in various herbs exhibit promising binding activities against the drug targets of multidrug resistant strains.

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